#4

1

SEQUENCE LISTING

<110> JORGE H. CAPDEVILA, MICHAEL WATERMAN, AND VIJAKUMAR HOLLA

<120> COMPOSITIONS AND METHODS RELATING TO
      HYPERTENSION

<130> 22000.0110U2

<150> 60/228,947
<151> 2000-08-29

<160> 9

<170> FastSEQ for Windows Version 4.0

<210> 1
<211> 4123
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence; Note =
      synthetic construct

<221> misc_feature
<222> (1)...(4123)
<223> n = g, a, c or t(u)

<400> 1
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ttgtaaaatg accacaaagt gggctaaaag ttcagacgta tggagcatgt ccctctcggt    180
ctttggtttt gaccaaagct cagaattgtg gaaagaaaga aaaagtagtg ggttatgcat    240
gttgtgtcac agtggaagat gaagtagtgg gtgttaaaga aaatgtttgg atagataaag    300
gatcaagtga gcggcaaaca cacattcctg gcagagtgaa tgggctggct ttctagagat    360
tcttgttaaa ataccttttg tgtttgcctc tttgtggtct tcacaactag gattaattta    420
gggaagataa tcatgatcca ggtgaggata aagattccag agaaaggctt atttctaccc    480
cttaacttct ttgttttttct tcctttctaa aagtttgtc atttttaaaa tttattttttt    540
atttaatttt tttcatgcaa tataatttga tcatattctt tccttcctcc aacttctcct    600
agatcctcag ggccttccta gctatccatc ttcatgttaa tggatagact gacaaccaaa    660
acattctttc tctgcttaaa taatatctcc ataaaatcta taaataaatg aggtagttgg    720
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aactttcgct ttatctattc tgtgtgnaca ttaatttttt tcaggcaagg cataatatat    840
atataattgg actgatttct ttattagagt ttgccctatg tgaggtcaag aaatattctt    900
aaattaatga gtgactgaat aagtgatggg caatttaagt atttagaaaa gaaaggtttt    960
attattccat tcagtcaaga tagtgagaca gagaaagagt ctgtcacagg ctgtgtatgt   1020
ggtgaggctg attgagtctt gagccacctg aatgcaactg cactgttcca cctgctggca   1080
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cagctggatt tggagtccag atgcaaagat gactataggt agaaactttc agcaattaca   1200
ttcatctgaa cacaccaact actgttgtca tcatttcacc ctgaaattag gaaaatagta   1260
caagcagcta cacctattac atgtttggta aattagaatg tgaatttctt aatatccagg   1320
ttaatgtcta gtccatgact ttacctcatc agcaaggata tacataacat gcaatatgtg   1380
ctcaataaat agttgtgagt agttcagaga aatgggaatt ggtatacata tagatgttac   1440
caagactaga tactagagat ttgtttttac tgtttaccaa agctgatgtt gcagattaat   1500
aaactttgga ttctgaggtc agtctctgtc tgtcttctcc attccccctc ccacaagtag   1560
gtgtgtctac cttctcatga cttaaatgcg ggtttctaaa catttagtga cactagtgat   1620
ccagaaacta ctaaccatgg gttttttttt atttagccct acaaggtact tggatggtat   1680
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ctctgggttc ttccaatggg ccttcttgct cagtctattt ctggtgctgt tcaaggcagt    1740
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ttcccactgg ctttgggggc accatctgaa gggacaagga gctccagcag attcttatat    1860
gggtagagaa attcccaagt gcctgcttac agtgtctctc ggggagcaat atacgagtcc    1920
tgctttatga tcctgactat gtgaaggtgg ttctggggag atcagatcca aaggcttctg    1980
gaatttatca attctttgct ccctggattg gttatggttt gctcctgttg aatgggaaga    2040
agtggttcca gcatcggcgg atgttgactc cagccttcca ctatgacatc ctcaaaccct    2100
atgtcaaaat catggcggac tctgtcaata taatgctaga taaatgggag aagcttgatg    2160
gccaggacca ccctctggag atcttccact gtgtttcatt gatgacactg gacactgtta    2220
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tacatcataa cccacgtttc tggccaaacc caaaggtgtt tgacccctct agatttgcac    2940
cagattcttc tcaccatagc catgcttatc tgccattctc aggaggatca aggaactgca    3000
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ccaagaatgg gatccacctg tgtctcaaga agctaagata attctgatgg agtcagggca    3180
gctccagagg tctgctgcct gcaatacctg cttttgtctc tggctttttct gtactttgct    3240
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cctcatttct gtagcttttc ctctagacac cttcctaacc tgtgcatgta cctgtttccc    3360
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ttcaccccct cataaccattg cactgacaga ggaagatata ttttagaggg agacacttgt    3480
acctttctct cccttcagtt attagactct tgggacaatg gacatcatga attaaaacgt    3540
tcttagaaat cacatgctgg gagaaaatta acactaaaat ctggtaccag ccagaggaag    3600
gaacttgact caaaataaga gatttttaga tatttctgtc tgtctcatag ttaaaattaa    3660
tgttttcctg ctttctggca tatgcctcat ctttttctatg aagtagtaat actgatacag    3720
aaaggtagag agaaatgaat agttttgct actttgggcc aaactgtgaa aaaatccatt    3780
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aactttgggg agccagagca gttttggcaa tccaggaag catgttgcca tctggtccct    3900
actgttagaa tgtggtagaa ttctcagctc ctgagaggtt gttctctgct tttgactcct    3960
gagctggttg tgtagaaatg caggttggcg ttttttgtga agctaaggag ttttctgact    4020
ttaacccggt cttatttgtt tagagtactc tgattattca ctttagtgat ttggagaatt    4080
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```

<210> 2
<211> 507
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence; Note =
      synthetic construct

<400> 2

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Met Gly Phe Phe Val Phe Ser Pro Thr Arg Tyr Leu Asp Gly Ile Ser
 1               5                   10                  15
Gly Phe Phe Gln Trp Ala Phe Leu Leu Ser Leu Phe Leu Val Leu Phe
                20                  25                  30
Lys Ala Val Gln Phe Tyr Leu Arg Arg Gln Trp Leu Leu Lys Thr Leu
        35                  40                  45
```

```
Gln His Phe Pro Cys Met Pro Ser His Trp Leu Trp Gly His His Leu
    50              55              60
Lys Asp Lys Glu Leu Gln Gln Ile Leu Ile Trp Val Glu Lys Phe Pro
65              70              75              80
Ser Ala Cys Leu Gln Cys Leu Ser Gly Ser Asn Ile Arg Val Leu Leu
            85              90              95
Tyr Asp Pro Asp Tyr Val Lys Val Val Leu Gly Arg Ser Asp Pro Lys
        100             105             110
Ala Ser Gly Ile Tyr Gln Phe Phe Ala Pro Trp Ile Gly Tyr Gly Leu
        115             120             125
Leu Leu Leu Asn Gly Lys Lys Trp Phe Gln His Arg Arg Met Leu Thr
    130             135             140
Pro Ala Phe His Tyr Asp Ile Leu Lys Pro Tyr Val Lys Ile Met Ala
145             150             155             160
Asp Ser Val Asn Ile Met Leu Asp Lys Trp Glu Lys Leu Asp Gly Gln
            165             170             175
Asp His Pro Leu Glu Ile Phe His Cys Val Ser Leu Met Thr Leu Asp
        180             185             190
Thr Val Met Lys Cys Ala Phe Ser Tyr Gln Gly Ser Val Gln Leu Asp
    195             200             205
Glu Asn Ser Lys Leu Tyr Thr Lys Ala Val Glu Asp Leu Asn Asn Leu
    210             215             220
Thr Phe Phe Arg Leu Arg Asn Ala Phe Tyr Lys Tyr Asn Ile Ile Tyr
225             230             235             240
Asn Met Ser Ser Asp Gly Arg Leu Ser His His Ala Cys Gln Ile Ala
            245             250             255
His Glu His Thr Asp Gly Val Ile Lys Met Arg Lys Ser Gln Leu Gln
        260             265             270
Asn Glu Glu Glu Leu Gln Lys Ala Arg Lys Lys Arg His Leu Asp Phe
    275             280             285
Leu Asp Ile Leu Leu Phe Ala Arg Met Glu Asp Arg Asn Ser Leu Ser
    290             295             300
Asp Glu Asp Leu Arg Ala Glu Val Asp Thr Phe Met Phe Glu Gly His
305             310             315             320
Asp Thr Thr Ala Ser Gly Ile Ser Trp Ile Phe Tyr Ala Leu Ala Thr
            325             330             335
His Pro Glu His Gln Gln Arg Cys Arg Glu Glu Val Gln Ser Ile Leu
        340             345             350
Gly Asp Gly Thr Ser Val Thr Trp Asp His Leu Gly Gln Met Pro Tyr
        355             360             365
Thr Thr Met Cys Ile Lys Glu Ala Leu Arg Leu Tyr Pro Pro Val Ile
    370             375             380
Ser Val Ser Arg Glu Leu Ser Ser Pro Val Thr Phe Pro Asp Gly Arg
385             390             395             400
Ser Ile Pro Lys Gly Ile Thr Ala Thr Ile Ser Ile Tyr Gly Leu His
            405             410             415
His Asn Pro Arg Phe Trp Pro Asn Pro Lys Val Phe Asp Pro Ser Arg
        420             425             430
Phe Ala Pro Asp Ser Ser His His Ser His Ala Tyr Leu Pro Phe Ser
        435             440             445
Gly Gly Ser Arg Asn Cys Ile Gly Lys Gln Phe Ala Met Asn Glu Leu
        450             455             460
Lys Val Ala Val Ala Leu Thr Leu Leu Arg Phe Glu Leu Leu Pro Asp
465             470             475             480
Pro Thr Arg Ile Pro Val Pro Ile Ala Arg Leu Val Leu Lys Ser Lys
            485             490             495
Asn Gly Ile His Leu Cys Leu Lys Lys Leu Arg
        500             505
```

<210> 3
<211> 508
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence; Note =
      synthetic construct

<400> 3
Met Ser Ala Ser Ala Leu Ser Ser Ile Arg Phe Pro Gly Ser Ile Ser
 1   5   10   15
Glu Tyr Leu Gln Val Ala Ser Val Leu Ser Leu Leu Leu Leu Leu Phe
            20   25   30
Lys Thr Ala Gln Leu Tyr Leu His Arg Gln Trp Leu Leu Ser Ser Thr
        35   40   45
Gln Gln Phe Pro Ser Pro Ser His Trp Leu Phe Gly His Lys Ile
    50   55   60
Leu Lys Asp Gln Asp Leu Gln Asp Ile Leu Thr Arg Ile Lys Asn Phe
65   70   75   80
Pro Ser Ala Cys Pro Gln Trp Leu Trp Gly Ser Lys Val Arg Ile Gln
                85   90   95
Val Tyr Asp Pro Asp Tyr Met Lys Leu Ile Leu Gly Arg Ser Asp Pro
               100   105   110
Lys Ala Asn Gly Ser Tyr Arg Phe Leu Ala Pro Trp Ile Gly Arg Gly
           115   120   125
Leu Leu Met Leu Asp Gly Gln Thr Trp Phe Gln His Arg Arg Met Leu
       130   135   140
Thr Pro Ala Phe His Tyr Asp Ile Leu Lys Pro Tyr Thr Glu Ile Met
145   150   155   160
Ala Asp Ser Val Arg Val Met Leu Asp Lys Trp Glu Gln Ile Val Gly
               165   170   175
Gln Asp Ser Thr Leu Glu Ile Phe Arg His Ile Thr Leu Met Thr Leu
           180   185   190
Asp Thr Ile Met Lys Cys Ala Phe Ser His Glu Gly Ser Val Gln Leu
       195   200   205
Asp Arg Lys Tyr Lys Ser Tyr Ile Gln Ala Val Glu Asp Leu Asn Asp
   210   215   220
Leu Val Phe Ser Arg Val Arg Asn Ile Phe His Leu Asn Asp Ile Ile
225   230   235   240
Tyr Arg Val Ser Ser Asn Gly Cys Lys Ala Asn Ser Ala Cys Gln Leu
               245   250   255
Ala His Asp His Thr Asp Gln Val Ile Lys Ser Arg Arg Ile Gln Leu
           260   265   270
Gln Asp Glu Glu Glu Leu Glu Lys Leu Lys Lys Lys Arg Arg Leu Asp
       275   280   285
Phe Leu Asp Ile Leu Leu Phe Ala Arg Met Glu Asn Gly Lys Ser Leu
   290   295   300
Ser Asp Lys Asp Leu Arg Ala Glu Val Asp Thr Phe Met Phe Glu Gly
305   310   315   320
His Asp Thr Thr Ala Ser Gly Ile Ser Trp Ile Phe Tyr Ala Leu Ala
               325   330   335
Thr Asn Pro Glu His Gln Gln Arg Cys Arg Lys Glu Ile Gln Ser Leu
           340   345   350
Leu Gly Asp Gly Thr Ser Ile Thr Trp Asn Asp Leu Asp Lys Met Pro
       355   360   365
Tyr Thr Thr Met Cys Ile Lys Glu Ala Leu Arg Ile Tyr Pro Pro Val
   370   375   380

```
Pro Ser Val Ser Arg Glu Leu Ser Ser Pro Val Thr Phe Pro Asp Gly
385             390             395                 400
Arg Ser Leu Pro Lys Gly Ile His Val Met Leu Ser Phe Tyr Gly Leu
            405             410                 415
His His Asn Pro Thr Val Trp Pro Asn Pro Glu Val Phe Asp Pro Ser
            420             425                 430
Arg Phe Ala Pro Gly Ser Ser Arg His Ser His Ser Phe Leu Pro Phe
        435             440                 445
Ser Gly Gly Ala Arg Asn Cys Ile Gly Lys Gln Phe Ala Met Asn Glu
        450             455             460
Leu Lys Val Ala Val Ala Leu Thr Leu Leu Arg Phe Glu Leu Leu Pro
465             470             475                 480
Asp Pro Thr Arg Val Pro Ile Pro Ile Pro Arg Ile Val Leu Lys Ser
            485             490                 495
Lys Asn Gly Ile His Leu His Leu Lys Glu Leu Gln
            500             505
```

<210> 4
<211> 2116
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence; Note =
      synthetic construct

<400> 4
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gaactgtttg gataaagtga caccactatt acctaatatg tctttcattt cattgctccc     120
caaagaggct gttcaggtcc atcaaccctg gtcttgaaat caagctctgc tcacacccct     180
ctccctcccc caagtaggtg gggcaaccct cctggggttt gcagacagga gggtgttcat     240
tgaaagtgaa ggagagttgg tgatccagaa gctgttgtat catgagtgcc tctgctctga     300
gctccatcag attcccagga agcatctctg agtaccttca agtagcctct gtgctcagcc     360
tgctcctgct gctcttcaag acagcccagc tctacctgca caggcaatgg ctactcagca     420
gtactcagca gttcccatcc ccaccttctc actggctctt ggacacaag atcttaaagg      480
accaggacct tcaagatatt ctaactagga ttaagaattt cccaagtgcc tgtccacagt     540
ggctctgggg aagcaaagtg cgcattcaag tgtatgaccc tgactacatg aagctgattc     600
tggggagatc agacccaaaa gctaatggtt cctacagatt ctagctccc tggattgggc      660
gtggtttgct tatgctggat ggacagacat ggtttcagca ccgacgaatg ttgaccccag     720
ctttccacta tgacattctg aagccttata cggaaatcat ggcagactct gttcgtgtaa     780
tgctggataa atgggaacag attgttggcc aggattccac cctggagatc tttcgacaca     840
tcaccttgat gaccttggac accatcatga agtgtgcctt cagccacgag ggcagtgtcc     900
agttggacag aaaatacaag tcctatatcc aggcagttga ggacctgaac gatctcgttt     960
tttcccgtgt gcggaacatc tttcacctga atgacatcat ctacagagtg tcctctaatg    1020
gctgcaaggc taacagtgcc tgcaaacttg cccatgatca cacagaccaa gtgatcaaat    1080
caaggaggat tcaacttcag gatgaggaag agttggaaaa gcttaagaag aaaaggcgat    1140
tggatttcct ggacatcctc ctatttgcca gaatggaaaa tggaaaaagc ttatctgata    1200
aggaccttcg tgctgaagtg gatactttca tgttcgaggg ccatgacacc acagctagtg    1260
gtatctcctg gatcttctat gctttggcca caaatcctga acatcaacag agatgcagga    1320
aggagatcca aagtctccta ggagatggga cttctatcac ctggaatgac ctggacaaga    1380
tgcctatac taccatgtgc atcaaggagg ccctgaggat ctaccctcct gtaccaagtg     1440
tgagcagaga gctcagctca cctgtcacct ttccagatgg acgttcttta cccaaaggta    1500
tccatgttat gctctccttt tatggccttc atcacaaccc aactgtgtgg ccaaatccag    1560
aggtgtttga tccttctcga tttgcaccag ggtcttcccg gcacagccac tcattcctgc    1620
ccttctcagg aggagcaagg aactgcattg ggaaacagtt gcgatgaat gagctgaagg     1680
tggctgtggc cctgaccctg ctccgctttg agctgctgcc agatcccacc agagtcccaa    1740
tccccatacc aagaattgtg ttgaagtcca gaatgggat ccacttgcat ctcaaagagc     1800
tccaataatc ttcacaggac aagacagctc aaatgcatgc tgcctgccat tctgtctttc    1860
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tgtcacttac tcttttcccc aatccttctg ctcacatctc attctttctt ctcaccttgt    1920
tcacctccac ccaccttctg ctgggcttcc agtctccttg cctgtcagtc tttttcaact    1980
tcttctgaga tccctacttg cttttctctc tacctgtccc taaccagact gcatgtttga    2040
cctttgactt taatgatctc cctaacttgc accctgcctt tcttttctgt gtatttcctt    2100
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```

<210> 5
<211> 519
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence; Note =
      synthetic construct

<400> 5

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Met Ser Val Ser Val Leu Ser Pro Ser Arg Leu Leu Gly Asp Val Ser
 1               5                  10                  15
Gly Ile Leu Gln Ala Ala Ser Leu Leu Ile Leu Leu Leu Leu Leu Ile
            20                  25                  30
Lys Ala Val Gln Leu Tyr Leu His Arg Gln Trp Leu Leu Lys Ala Leu
        35                  40                  45
Gln Gln Phe Pro Cys Pro Pro Ser His Trp Leu Phe Gly His Ile Gln
    50                  55                  60
Glu Leu Gln Gln Asp Gln Glu Leu Gln Arg Ile Gln Lys Trp Val Glu
65                  70                  75                  80
Thr Phe Pro Ser Ala Cys Pro His Trp Leu Trp Gly Gly Lys Val Arg
                85                  90                  95
Val Gln Leu Tyr Asp Pro Asp Tyr Met Lys Val Ile Leu Gly Arg Ser
            100                 105                 110
Asp Pro Lys Ser His Gly Ser Tyr Arg Phe Leu Ala Pro Trp Ile Gly
        115                 120                 125
Tyr Gly Leu Leu Leu Leu Asn Gly Gln Thr Trp Phe Gln His Arg Arg
    130                 135                 140
Met Leu Thr Pro Ala Phe His Tyr Asp Ile Leu Lys Pro Tyr Val Gly
145                 150                 155                 160
Leu Met Ala Asp Ser Val Arg Val Met Leu Asp Lys Trp Glu Glu Leu
                165                 170                 175
Leu Gly Gln Asp Ser Pro Leu Glu Val Phe Gln His Val Ser Leu Met
            180                 185                 190
Thr Leu Asp Thr Ile Met Lys Cys Ala Phe Ser His Gln Gly Ser Ile
        195                 200                 205
Gln Val Asp Arg Asn Ser Gln Ser Tyr Ile Gln Ala Ile Ser Asp Leu
    210                 215                 220
Asn Asn Leu Val Phe Ser Arg Val Arg Asn Ala Phe His Gln Asn Asp
225                 230                 235                 240
Thr Ile Tyr Ser Leu Thr Ser Ala Gly Arg Trp Thr His Arg Ala Cys
                245                 250                 255
Gln Leu Ala His Gln His Thr Asp Gln Val Ile Gln Leu Arg Lys Ala
            260                 265                 270
Gln Leu Gln Lys Glu Gly Glu Leu Glu Lys Ile Lys Arg Lys Arg His
        275                 280                 285
Leu Asp Phe Leu Asp Ile Leu Leu Leu Ala Lys Met Glu Asn Gly Ser
    290                 295                 300
Ile Leu Ser Asp Lys Asp Leu Arg Ala Glu Val Asp Thr Phe Met Phe
305                 310                 315                 320
Glu Gly His Asp Thr Thr Ala Ser Gly Ile Ser Trp Ile Leu Tyr Ala
                325                 330                 335
```

```
Leu Ala Thr His Pro Lys His Gln Glu Arg Cys Arg Glu Glu Ile His
        340             345             350
Ser Leu Leu Gly Asp Gly Ala Ser Ile Thr Trp Asn His Leu Asp Gln
        355             360             365
Met Pro Tyr Thr Thr Met Cys Ile Lys Glu Ala Leu Arg Leu Tyr Pro
        370             375             380
Pro Val Pro Gly Ile Gly Arg Glu Leu Ser Thr Pro Val Thr Phe Pro
385             390             395             400
Asp Gly Arg Ser Leu Pro Lys Gly Ile Met Val Leu Leu Ser Ile Tyr
            405             410             415
Gly Leu His His Asn Pro Lys Val Trp Pro Asn Pro Glu Val Phe Asp
            420             425             430
Pro Phe Arg Phe Ala Pro Gly Ser Ala Gln His Ser His Ala Phe Leu
        435             440             445
Pro Phe Ser Gly Gly Ser Arg Asn Cys Ile Gly Lys Gln Phe Ala Met
        450             455             460
Asn Glu Leu Lys Val Ala Thr Ala Leu Thr Leu Leu Arg Phe Glu Leu
465             470             475             480
Leu Pro Asp Pro Thr Arg Ile Pro Ile Pro Ile Ala Arg Leu Val Leu
            485             490             495
Lys Ser Lys Asn Gly Ile His Leu Arg Leu Arg Arg Leu Pro Asn Pro
            500             505             510
Cys Glu Asp Lys Asp Gln Leu
        515
```

<210> 6
<211> 2576
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence; Note =
      synthetic construct

<400> 6
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tgctgatcaa ggcagttcag ctctacctgc acaggcagtg gctgctcaaa gccctccagc   180
agttcccgtg ccctccctcc cactggctct cgggcacat ccaggagctc caacaggacc    240
aggagctaca acggattcag aaatgggtgg agacattccc aagtgcctgt cctcattggc   300
tatggggagg caaagttcgt gtccagctct atgaccctga ctatatgaag gtgattctgg   360
ggagatcaga cccgaaatcc catggttcct acagattcct ggctccatgg attgggtacg   420
gcttgctcct gttgaatggg cagacatggt tccagcatcg acggatgctg accccagcct   480
tccactatga catcctgaag ccctatgtgg ggctcatggc agactctgta cgagtgatgc   540
tggacaaatg ggaagagctc cttggccagg attcccctct ggaggtcttt cagcacgtct   600
ccttgatgac cctggacacc atcatgaagt gtgccttcag ccatcagggc agcatccagg   660
tggacaggaa ttctcagtcc tacatacagg ccattagtga cctgaacaac ctggtttttt   720
cccgtgtgag gaatgccttt caccagaatg acaccatcta cagcctgacc tctgctggcc   780
gctggacaca ccgcgcctgc cagctggccc atcagcacac agaccaagtg atccaactga   840
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acctccgtgc tgaggtggac acgttcatgt ttgagggcca cgacaccaca gccagtggga  1020
tctcctggat cctctatgct ctggccacac accccaagca tcaggagagg tgccgggagg  1080
agatccacag cctcctgggt gatggagcct ccatcacctg gaaccacctg accagatgc   1140
cctacaccac catgtgcatt aaggaggcac tgaggctcta cccaccggtg ccaggcattg  1200
gcagagagct cagcactccc gtcaccttcc ctgatgggcg ctccttgccc aaaggtatca  1260
tggtcctcct ctccatttat ggccttcacc acaacccaaa agtgtggccc aacccagagg  1320
tgtttgaccc tttccgtttt gcaccgggtt ctgctcaaca cagccacgct ttcctgccct  1380
```

```
tctcaggagg atcaaggaac tgcattggga aacaatttgc catgaacgag ctgaaggtgg    1440
ccacggccct gaccctgctc cgctttgagc tgctgcctga tcccaccagg atccccatcc    1500
ccattgcacg acttgtgttg aaatccaaaa atggaatcca cctgcgtctc aggaggctcc    1560
ctaacccttg tgaagacaag gaccagcttt gagggcctcc acctgccgtc ctgtcttcct    1620
gacccccgct tctgtcccct tcctgtctgc ccatatcctg ttttctgtct gcccaccttc    1680
ccttcttccc acctgcctgc tgtcccccag tctgcctgcc cttctctctc tcacctttct    1740
ccaggctccc tacctgcttg tctacctgtc tcctacccac ctgtatctct tgttgggaga    1800
aaagctgagt gttgggagaa gctgaggccg agcttgcatg tctgacataa tgtaaaagag    1860
tcttgaatca tgtccaggat ccagggtcta aaaccccttg tggcctttgg aacaccaagc    1920
tctgtgctga agggtggaag ctaccctga cgcaccataa tctaagcccg gggcataaaa    1980
cccctcgtgg cttggataga atccagggct cgtggctctg aatgtgtct ggacttgctg    2040
gctccttgct ccttgctctc ccaggatcaa ttgtatcttg agttaaaaga acctgctctc    2100
cattatctca agtaacagag cagatgctaa accgtcacag ctgtaaattg tgtgcttaat    2160
gcaacatgcc ctttcgaccc accccccatt ctcaccacct gtttctttgt ttgatcacca    2220
ataaataatc tgcacttcca gagctcgggg ccttcacagc ctccatcctt agctttggcg    2280
ccctggaccc actttctctc tcaaactgtc ttttctcact gctttgactc tgccggactt    2340
tgtcacccc acgacctggt gttgggtctg aacaccccaa catccctgaa tctccaccca    2400
cctcccaaac tcctgcctgc cctccagact gtctgcccat acacctgtct ccttcttcct    2460
gcctggcttg tctgttccta tattagtttc ctattactgc tgtaataaac tatcacaatc    2520
tcagtgattt taaataaaaa aaaaaaaaa aaaaaaaaa aaaaaaacg gaattc          2576
```

\<210> 7
\<211> 519
\<212> PRT
\<213> Artificial Sequence

\<220>
\<223> Description of Artificial Sequence; Note =
     synthetic construct

\<400> 7

```
Met Ser Val Ser Val Leu Ser Pro Ser Arg Arg Leu Gly Gly Val Ser
1               5                   10                  15
Gly Ile Leu Gln Val Thr Ser Leu Leu Ile Leu Leu Leu Leu Leu Ile
            20                  25                  30
Lys Ala Ala Gln Leu Tyr Leu His Arg Gln Trp Leu Leu Lys Ala Leu
        35                  40                  45
Gln Gln Phe Pro Cys Pro Pro Ser His Trp Leu Phe Gly His Ile Gln
    50                  55                  60
Glu Phe Gln His Asp Gln Glu Leu Gln Arg Ile Gln Glu Arg Val Lys
65                  70                  75                  80
Thr Phe Pro Ser Ala Cys Pro Tyr Trp Ile Trp Gly Gly Lys Val Arg
                85                  90                  95
Val Gln Leu Tyr Asp Pro Asp Tyr Met Lys Val Ile Leu Gly Arg Ser
            100                 105                 110
Asp Pro Lys Ser His Gly Ser Tyr Arg Phe Leu Ala Pro Arg Ile Gly
        115                 120                 125
Tyr Gly Leu Leu Leu Leu Asn Gly Gln Thr Trp Phe Gln His Arg Arg
    130                 135                 140
Met Leu Thr Pro Ala Phe His Asn Asp Ile Leu Lys Pro Tyr Val Gly
145                 150                 155                 160
Leu Met Ala Asp Ser Val Arg Val Met Leu Asp Lys Trp Glu Glu Leu
                165                 170                 175
Leu Gly Gln Asp Ser Pro Leu Glu Val Phe Gln His Val Ser Leu Met
            180                 185                 190
Thr Leu Asp Thr Ile Met Lys Ser Ala Phe Ser His Gln Gly Ser Ile
        195                 200                 205
Gln Val Asp Arg Asn Ser Gln Ser Tyr Ile Gln Ala Ile Ser Asp Leu
```

```
            210                  215                  220
Asn Ser Leu Val Phe Cys Cys Met Arg Asn Ala Phe His Glu Asn Asp
225                  230                  235                  240
Thr Ile Tyr Ser Leu Thr Ser Ala Gly Arg Trp Thr His Arg Ala Cys
                245                  250                  255
Gln Leu Ala His Gln His Thr Asp Gln Val Ile Gln Leu Arg Lys Ala
                260                  265                  270
Gln Leu Gln Lys Glu Gly Glu Leu Glu Lys Ile Lys Arg Lys Arg His
            275                  280                  285
Leu Asp Phe Leu Asp Ile Leu Leu Leu Ala Lys Met Glu Asn Gly Ser
        290                  295                  300
Ile Leu Ser Asp Lys Asp Leu Arg Ala Glu Val Asp Thr Phe Met Phe
305                  310                  315                  320
Glu Gly His Asp Thr Thr Ala Ser Gly Ile Ser Trp Ile Leu Tyr Ala
                325                  330                  335
Leu Ala Thr His Pro Lys His Gln Glu Arg Cys Arg Glu Glu Ile His
                340                  345                  350
Gly Leu Leu Gly Asp Gly Ala Ser Ile Thr Trp Asn His Leu Asp Gln
            355                  360                  365
Met Pro Tyr Thr Thr Met Cys Ile Lys Glu Ala Leu Arg Leu Tyr Pro
    370                  375                  380
Pro Val Pro Gly Ile Gly Arg Glu Leu Ser Thr Pro Val Thr Phe Pro
385                  390                  395                  400
Asp Gly Arg Ser Leu Pro Lys Gly Ile Met Val Leu Leu Ser Ile Tyr
                405                  410                  415
Gly Leu His His Asn Pro Lys Val Trp Pro Asn Leu Glu Val Phe Asp
                420                  425                  430
Pro Ser Arg Phe Ala Pro Gly Ser Ala Gln His Ser His Ala Phe Leu
            435                  440                  445
Pro Phe Ser Gly Gly Ser Arg Asn Cys Ile Gly Lys Gln Phe Ala Met
        450                  455                  460
Asn Gln Leu Lys Val Ala Arg Ala Leu Thr Leu Leu Arg Phe Glu Leu
465                  470                  475                  480
Leu Pro Asp Pro Thr Arg Ile Pro Ile Pro Ile Ala Arg Leu Val Leu
                485                  490                  495
Lys Ser Lys Asn Gly Ile His Leu Arg Leu Arg Arg Leu Pro Asn Pro
            500                  505                  510
Cys Glu Asp Lys Asp Gln Leu
        515


<210> 8
<211> 1872
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence; Note =
      synthetic construct

<400> 8
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gctgttctcc cactgttccc ctaggtggat catccaaagt caatcgattc tgaactctga     180
ggtccaagtt ctgccctccc ccttcactct ccccacaagt gggcgggaca atcctcccat     240
gacttaagca caggtggaca ggggtggtca gagagaggaa ggggcactca gagatccagc     300
aggtgctgca ccatgagtgt ctctgtcctg agccccagca gacgcctggg tggtgtctcc     360
gggatcctcc aagtgacctc cctgctcatt ctgcttctgc tgctgatcaa ggcagctcag     420
ctctacctgc ataggcagtg gctgctcaaa gccctccagc agttcccgtg ccctccctcc     480
```

```
cactggctct tcgggcacat ccaggagttc caacacgacc aggagctaca acggattcag    540
gaacgggtga agacattccc aagtgcctgt ccttattgga tatggggagg caaagttcgt    600
gtccagctct atgaccctga ctatatgaag gtgattctgg ggagatcaga cccgaaatcc    660
catggttcct acagattcct ggctccacgg attgggtacg gcttgctcct gttgaatggg    720
cagacatggt tccagcatcg acggatgctg accccagcct tccacaatga catcctgaag    780
ccatatgtgg ggctcatggc agactctgta cgagtgatgc tggacaaatg ggaagagctc    840
cttggccagg attcccctct ggaggtcttt cagcacgtct ccttgatgac cctggacacc    900
atcatgaaga gtgccttcag ccatcagggc agcatccagg tggacaggaa ttctcagtcc    960
tacatccagg ccattagtga cctgaacagc ctggtttttt gctgtatgag gaatgccttt   1020
catgagaatg acaccatcta cagcctgacc tctgctggcc gctggacaca ccgcgcctgc   1080
cagctggccc atcagcacac agaccaagtg atccaactga ggaaggctca actacagaag   1140
gaggggggagc tggagaagat caagaggaag aggcacttgg attttctgga catcctcctc   1200
ttggccaaaa tggagaatgg gagcatcttg tcagacaagg acctccgtgc tgaggtggac   1260
acgttcatgt ttgagggcca cgacaccaca gccagtggga tctcctggat cctctatgct   1320
ctggccacac accccaagca tcaggagagg tgccgggagg agatccatgg cctcctgggt   1380
gatggagcct ccatcacctg gaaccacctg gaccagatgc cctacaccac catgtgcatt   1440
aaggaggcac tgaggctcta cccaccggtg ccaggcattg gaagagagct cagcactccc   1500
gtcaccttcc ctgatgggcg ctccttgccc aaaggtatca tggtcctcct ctccatttat   1560
ggccttcacc acaacccaaa agtgtggccc aacctagagg tgtttgaccc ttcccgtttt   1620
gcaccgggtt ctgctcaaca cagccacgct ttcctgccct tctcaggagg atcaaggaac   1680
tgcatcggga aacaatttgc catgaaccag ctgaaggtgg ccagggccct gaccctgctc   1740
cgctttgagc tgctgcctga tcccaccagg atccccatcc ccattgcacg acttgtgttg   1800
aaatccaaaa atggaatcca cctgcgtctc aggaggctcc ctaacccttg tgaagacaag   1860
gaccagcttt ga                                                       1872
```

<210> 9
<211> 21990
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence; Note =
      synthetic construct

<221> misc_feature
<222> (1)...(21990)
<223> n = g, a, c or t(u)

<400> 9

```
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nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn    120
nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn    180
nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn    240
nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn    300
nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn    360
nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn    420
nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn    480
nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn    540
nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn    600
nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn    660
nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn    720
nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn    780
nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn    840
nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn    900
nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn    960
nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn   1020
nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn   1080
nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn   1140
```

```
nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn    1200
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nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn    1320
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nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn    2820
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```

```
nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn   4680
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nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn    20160
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nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn    20520
nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn    20580
nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn    20640
nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn    20700
nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn    20760
nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn    20820
nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn    20880
nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn    20940
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nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn    21060
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nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn    21180
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nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn    21300
nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn    21360
nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn    21420
nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn    21480
nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn    21540
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nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn    21660
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nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn    21840
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nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn    21960
nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn                                    21990
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